



Blast 2 Sequences results

PubMed

Entrez

BLAST

OMIM

Taxonomy

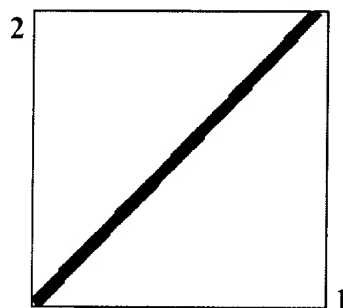
Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.5 [Nov-16-2002]

Matrix: **BLOSUM62** gap open: **11** gap extension: **1**
 x_dropoff: **30** expect: **10.000** wordsize: **3** Filter ☒ **Align**

Sequence 1 gi 829285 glutamine synthetase [Pisum sativum] **Length** 373 (1 .. 373)

Sequence 2 gi 404327 glutamate--ammonia ligase [Pinus sylvestris] **Length** 357 (1 .. 357)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 541 bits (1395), Expect = e-153

Identities = 250/351 (71%), Positives = 294/351 (83%)

```

Query: 7  DLLNLDITPFTDSITAEYIWI GGTGIDVESHSEITISKPVSHPSEVPFWNYDGSSTGQAP 66
        DLLNLD++ T+ +IAEYIWI GG+G+D+ESH+R++S PVS E+PFWNYDGSSTGQA G
Sbjct: 7  DLLNLDLSDVTEKVI AEYIWI GSGGMMMSHARSLSGPVSSVKELPFWNYDGSSTGQAQ 66

Query: 67 EDSEVILYPQAIIFKDPFRSGNNILWVCDAYTPAGEPIPTNKRHRAARIFSNPKVEASIPW 126
        DSEVILYPQAIIF+DPR G +ILV-CDAY+P G IP+NKR AA+IF+ V E W
Sbjct: 67 HDSEVILYPQAIIFRDPFRRGKHILVLCDAYSPNGTAIPSNKRAAAAKTFNEKAVSDRETW 126

Query: 127 YGIEQEYTLTQTNVKWPPLGWPVXXXXXXXXXXXXXXXXXDFSGGRDISDAHYPACIYAGIN 186
        YG+EQEYTLTQ +VWPLGWP- DF++GRDI DAHYPAC+Y+GIN
Sbjct: 127 YGLEQEYTLTQFDVWPLGWPFGGYPGPGGFEYTCGUGADKAWGFDIVDAHYPACLYSGIN 186

Query: 187 ISGTNGEWMPPGQWEYQVGPSVGI EACDHIWASHYILERITEQAGVVLTLDPFPIEGLWNG 246
        ISG NGEVMPGQWE+QVGPSVGI A D +W +F+I+ERITE+AGVVL+ DPYPIEGLWNG
Sbjct: 187 ISG:NGEVMPPGQWEI+QVGPSVGI SAADHLCAPFIMERITEKAGVVLSFDPEPEIEGLWNG 246

Query: 247 AGCHTNYSTKEMREDGGFEVIKKAHLNLSIRHKIHIEAYGEGNERRLTGKHETASINDFS 306
        AGCHTNYSTKEMR++GGFEVIKKA L LRHK HI AYGEGNERRLTG+HETA +N FS
Sbjct: 247 AGCHTNYSTKEMRKEGGFEVIKKAIEFLKLRHKEHISAYGEGNERRLTGPHETADKNTFS 306

Query: 307 WGVANRGCSIRVGRDTEKNGKGYLEDRRPASNMDFYVVTALLAESTLLWEP 357
        WGVANRG S+RVGRDTEK GKGY EDRPASNMDFY+VT+++AE+T+LW+P
Sbjct: 307 WGVANRGASRVGRDTEKECKGYFEDRRPASNMDFYIVTSMIAETTLWKP 357
  
```

CPU time: 0.09 user secs. 0.02 sys. secs 0.11 total secs.

Lambda	K	H
0.115	2.136	0.417

Gapped

Lambda	K	H
0.267	0.9410	0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Hits to DB: 1090

Number of Sequences: 0

Number of extensions: 73

Number of successful extensions: 2

Number of sequences better than 10.0: 1

Number of HSP's better than 10.0 without gapping: 1

Number of HSP's successfully gapped in prelim test: 0

Number of HSP's that attempted gapping in prelim test: 0

Number of HSP's gapped (non-prelim): 1

Length of query: 373

Length of database: 445,599,717

Effective HSP length: 128

Effective length of query: 245

Effective length of database: 445,599,589

Effective search space: 109171899305

Effective search space used: 109171899305

T: 9

A: 40

X1: 16 (7.3 bits)

X2: 77 (29.7 bits)

X3: 77 (29.7 bits)

S1: 42 (22.0 bits)

S2: 75 (33.5 bits)



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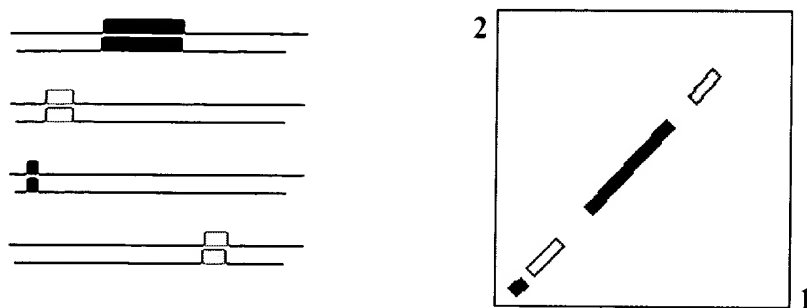
BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.5 [Nov-16-2002]

Match: Mismatch: gap open: gap extension:
 x_dropoff: expect: wordsize: Filter ☒ **Align**

Sequence 1 gi 404326 P.sylvestris mRNA for glutamine synthetase

Length 1423 (1 .. 1423)

Sequence 2 gi 20752 Pea leaf mRNA for glutamine synthetase (EC 6.3.1.2) **Length** 1304 (1 .. 1304)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

NOTE: If protein translation is reversed, please repeat the search with reverse strand of the query sequence

Score = 160 bits (93), Expect = 6e-46
 Identities = 285/386 (73%)
 Strand = Plus / Plus

Query: 454 aaatggcctcttggctggccaattgggtggctaccccggtctcagggcccatattact
 Sbjet: 423 aaatggccattaggttggcctgtagggtggctaccccggtctcagggctcattact
 glutamine synthetase 141 K W P L G W P V G G Y P G P Q G P Y Y

Query: 514 qqagttggagctgacaaagcctggggagagacattgttgatgccattataaggctt
 Sbjet: 483 gctgacggagagagataagtcatttggacgtgatatabctgatgctcattacaaggctt
 glutamine synthetase 161 A A G A D K S F G R D I S D A H Y K A

Query: 574 ctctatttcaggaatcaatatcagtggtcatcaatggagaagtcagggcaggtggg
 Sbjet: 543 atatatgctggaattacattagtggaaccaatggagaagttatgctggacagtggtg
 glutamine synthetase 181 I Y A G I N I S G T N G E V M P G Q W

Query: 634 tttcaagtaggttcgtcagtggggtatctcagbaggagatgagctgtgggtgtgctggtt

$$\text{Standard} = \frac{W_1 W_2}{W_1 + W_2}$$

```

Query:          945  ctttttcttgggggtgttgcaaatcgaggagcttcagtttagagtggggccggggacacaga
                ||||| ||||| || || || || || || || || || || || || || || || ||
Sbjct:          914  ctttttcttggggagtggttaaccgggggatgctcaatccgtgtgggaagagacaccga
glutamine synthetase 305  F S W G V A N R G C S I R V G R D T E

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Query:          1005  agaaggaaaagggttattttgaggaccgtcgacctgcttcaaacatggatccata 10
                ||| ||||| || || || || || || || || || || || || || || || ||
Sbjct:          974  gaatggcaagggttacttggaagacaggcggtccggcttcgaacatggatccata 10
glutamine synthetase 325  N S K G Y L E D R R P A S N M D P Y

```

CPU time: 0.03 user secs. 0.07 sys. secs 0.15 total secs.

Lambda K H
1.33 0.621 1.13

Gapped
Lambda K H
1.33 0.621 1.13

Matrix: blastn matrix:1 -2
 Gap Penalties: Existence: 5, Extension: 2
 Number of Hits to DB: 5
 Number of Sequences: 0
 Number of extensions: 5
 Number of successful extensions: 5
 Number of sequences better than 10.0: 1
 Number of HSP's better than 10.0 without gapping: 1
 Number of HSP's successfully gapped in prelim test: 0
 Number of HSP's that attempted gapping in prelim test: 0
 Number of HSP's gapped (non-prelim): 4
 Length of query: 1425
 Length of database: 7,976,531,563
 effective HSP length: 25
 effective length of query: 1396
 effective length of database: 7,976,531,538
 effective search space: 11151191090124
 effective search space used: 11151191090124
 T: 0
 A: 0
 X1: 7 (11.5 bits)
 X2: 26 (50.0 bits)
 S1: 12 (23.8 bits)
 S2: 21 (41.1 bits)